

03CC 10-25-96  
TEAM 5  
#3  
RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/704,159DATE: 10/28/96  
TIME: 17:40:00

INPUT SET: S13439.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: Williams, James A.  
Thalley, Bruce S.(ii) TITLE OF INVENTION: Multivalent Vaccine For Clostridium  
Botulinum Neurotoxin

(iii) NUMBER OF SEQUENCES: 82

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Medlen & Carroll  
(B) STREET: 220 Montgomery Street, Suite 2200  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: United States of America  
(F) ZIP: 94104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ingolia, Diane E.  
(B) REGISTRATION NUMBER: 40,027  
(C) REFERENCE/DOCKET NUMBER: OPHD-02304

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 705-8410  
(B) TELEFAX: (415) 397-8338

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single  
48 (D) TOPOLOGY: linear

49 (ii) MOLECULE TYPE: DNA (genomic)  
50  
51  
52

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
54  
55

24

56 GGAAATTTAG CTGCAGCATC TGAC  
57

58 (2) INFORMATION FOR SEQ ID NO:2:  
59

60 (i) SEQUENCE CHARACTERISTICS:  
61 (A) LENGTH: 24 base pairs  
62 (B) TYPE: nucleic acid  
63 (C) STRANDEDNESS: single  
64 (D) TOPOLOGY: linear

65 (ii) MOLECULE TYPE: DNA (genomic)  
66  
67

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
69  
70

24

71 TCTAGCAAAT TCGCTTGTGT TGAA  
72

73 (2) INFORMATION FOR SEQ ID NO:3:  
74

75 (i) SEQUENCE CHARACTERISTICS:  
76 (A) LENGTH: 20 base pairs  
77 (B) TYPE: nucleic acid  
78 (C) STRANDEDNESS: single  
79 (D) TOPOLOGY: linear

80 (ii) MOLECULE TYPE: DNA (genomic)  
81  
82

83 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
84  
85

20

86 CTGCGCATATA GCATTAGACC  
87  
88

89 (2) INFORMATION FOR SEQ ID NO:4:  
90

91 (i) SEQUENCE CHARACTERISTICS:  
92 (A) LENGTH: 19 base pairs  
93 (B) TYPE: nucleic acid  
94 (C) STRANDEDNESS: single  
95 (D) TOPOLOGY: linear

96 (ii) MOLECULE TYPE: DNA (genomic)  
97  
98

99

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100  
101  
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: 19  
103  
104 CTATCTAGGC CTAAAGTAT  
105  
106 (2) INFORMATION FOR SEQ ID NO:5:  
107  
108 (i) SEQUENCE CHARACTERISTICS:  
109 (A) LENGTH: 8133 base pairs  
110 (B) TYPE: nucleic acid  
111 (C) STRANDEDNESS: single  
112 (D) TOPOLOGY: linear  
113  
114 (ii) MOLECULE TYPE: DNA (genomic)  
115  
116  
117 (ix) FEATURE:  
118 (A) NAME/KEY: CDS  
119 (B) LOCATION: 1..8130  
120  
121 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
122  
123  
124 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT 48  
125 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile 15  
126 1 5 10  
127  
128 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA 96  
129 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu 30  
130 20 25  
131  
132 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA 144  
133 Tyr Asn Lys Leu Thr Thr Asn Asn Asn Glu Asn Lys Tyr Leu Gln Leu 45  
134 35 40  
135  
136 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT 192  
137 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr 60  
138 50 55  
139  
140 TCA AGC AGA AAT AGA GCA CTC TCT AAT CTA AAA AAA GAT ATA TTA AAA 240  
141 Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys 75 80  
142 65 70  
143  
144 GAA GTA ATT CTT ATT AAA AAT TCC AAT ACA AGC CCT GTA GAA AAA AAT 288  
145 Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn 95  
146 85 90  
147  
148 TTA CAT TTT GTA TGG ATA GGT GGA GAA GTC AGT GAT ATT GCT CTT GAA 336  
149 Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu 110  
150 100 105  
151  
152 TAC ATA AAA CAA TGG GCT GAT ATT AAT GCA GAA TAT AAT ATT AAA CTG 384

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153	Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu	125	
154	115	120	
155			432
156	TGG TAT GAT AGT GAA GCA TTC TTA GTA AAT ACA CTA AAA AAG GCT ATA		
157	Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile	140	
158	130	135	
159			480
160	GTT GAA TCT TCT ACC ACT GAA GCA TTA CAG CTA CTA GAG GAA GAG ATT		
161	Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Glu Ile	155	160
162	145	150	
163			528
164	CAA AAT CCT CAA TTT GAT AAT ATG AAA TTT TAC AAA AAA AGG ATG GAA		
165	Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu	170	175
166	165		
167			576
168	TTT ATA TAT GAT AGA CAA AAA AGG TTT ATA AAT TAT TAT AAA TCT CAA		
169	Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln	185	190
170	180		
171			624
172	ATC AAT AAA CCT ACA GTA CCT ACA ATA GAT GAT ATT ATA AAG TCT CAT		
173	Ile Asn Lys Pro Thr Val Pro Thr Ile Asp Asp Ile Ile Lys Ser His	200	205
174	195		
175			672
176	CTA GTA TCT GAA TAT AAT AGA GAT GAA ACT GTA TTA GAA TCA TAT AGA		
177	Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg	215	220
178	210		
179			720
180	ACA AAT TCT TTG AGA AAA ATA AAT AGT AAT CAT GGG ATA GAT ATC AGG		
181	Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg	230	235
182	225		
183			768
184	GCT AAT AGT TTG TTT ACA GAA CAA GAG TTA TTA AAT ATT TAT AGT CAG		
185	Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln	245	250
186	245		
187			816
188	GAG TTG TTA AAT CGT GGA AAT TTA GCT GCA GCA TCT GAC ATA GTA AGA		
189	Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ser Asp Ile Val Arg	260	265
190	260		
191			864
192	TTA TTA GCC CTA AAA AAT TTT GGC GGA GTA TAT TTA GAT GTT GAT ATG		
193	Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met	275	280
194	275		
195			912
196	CTT CCA GGT ATT CAC TCT GAT TTA TTT AAA ACA ATA TCT AGA CCT AGC		
197	Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser	290	295
198	290		
199			960
200	TCT ATT GGA CTA GAC CGT TGG GAA ATG ATA AAA TTA GAG GCT ATT ATG		
201	Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met	305	310
202	305		
203			1008
204	AAG TAT AAA AAA TAT ATA AAT AAT TAT ACA TCA GAA AAC TTT GAT AAA		
205	Lys Tyr Lys Lys Tyr Ile Asn Asn Tyr Thr Ser Glu Asn Phe Asp Lys		

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	325	330	335	
206				
207				
208	CTT GAT CAA CAA TTA AAA GAT AAT TTT AAA CTC ATT ATA GAA AGT AAA			1056
209	Leu Asp Gln Gln Leu Lys Asp Asn Phe Lys Leu Ile Ile Glu Ser Lys			
210		340	345	350
211				
212	AGT GAA AAA TCT GAG ATA TTT TCT AAA TTA GAA AAT TTA AAT GTA TCT			1104
213	Ser Glu Lys Ser Glu Ile Phe Ser Lys Leu Glu Asn Leu Asn Val Ser			
214		355	360	365
215				
216	GAT CTT GAA ATT AAA ATA GCT TTC GCT TTA GGC AGT GTT ATA AAT CAA			1152
217	Asp Leu Glu Ile Lys Ile Ala Phe Ala Leu Gly Ser Val Ile Asn Gln			
218		370	375	380
219				
220	GCC TTG ATA TCA AAA CAA GGT TCA TAT CTT ACT AAC CTA GTA ATA GAA			1200
221	Ala Leu Ile Ser Lys Gln Gly Ser Tyr Leu Thr Asn Leu Val Ile Glu			
222		385	390	395
223				
224	CAA GTA AAA AAT AGA TAT CAA TTT TTA AAC CAA CAC CTT AAC CCA GCC			1248
225	Gln Val Lys Asn Arg Tyr Gln Phe Leu Asn Gln His Leu Asn Pro Ala			
226		405	410	415
227				
228	ATA GAG TCT GAT AAT AAC TTC ACA GAT ACT ACT AAA ATT TTT CAT GAT			1296
229	Ile Glu Ser Asp Asn Asn Phe Thr Asp Thr Thr Lys Ile Phe His Asp			
230		420	425	430
231				
232	TCA TTA TTT AAT TCA GCT ACC GCA GAA AAC TCT ATG TTT TTA ACA AAA			1344
233	Ser Leu Phe Asn Ser Ala Thr Ala Glu Asn Ser Met Phe Leu Thr Lys			
234		435	440	445
235				
236	ATA GCA CCA TAC TTA CAA GTA GGT TTT ATG CCA GAA GCT CGC TCC ACA			1392
237	Ile Ala Pro Tyr Leu Gln Val Gly Phe Met Pro Glu Ala Arg Ser Thr			
238		450	455	460
239				
240	ATA AGT TTA AGT GGT CCA GGA GCT TAT GCG TCA GCT TAC TAT GAT TTC			1440
241	Ile Ser Leu Ser Gly Pro Gly Ala Tyr Ala Ser Ala Tyr Tyr Asp Phe			
242		465	470	475
243				
244	ATA AAT TTA CAA GAA AAT ACT ATA GAA AAA ACT TTA AAA GCA TCA GAT			1488
245	Ile Asn Leu Gln Glu Asn Thr Ile Glu Lys Thr Leu Lys Ala Ser Asp			
246		485	490	495
247				
248	TTA ATA GAA TTT AAA TTC CCA GAA AAT AAT CTA TCT CAA TTG ACA GAA			1536
249	Leu Ile Glu Phe Lys Phe Pro Glu Asn Asn Leu Ser Gln Leu Thr Glu			
250		500	505	510
251				
252	CAA GAA ATA AAT AGT CTA TGG AGC TTT GAT CAA GCA AGT GCA AAA TAT			1584
253	Gln Glu Ile Asn Ser Leu Trp Ser Phe Asp Gln Ala Ser Ala Lys Tyr			
254		515	520	525
255				
256	CAA TTT GAG AAA TAT GTA AGA GAT TAT ACT GGT GGA TCT CTT TCT GAA			1632
257	Gln Phe Glu Lys Tyr Val Arg Asp Tyr Thr Gly Gly Ser Leu Ser Glu			
258		530	535	540